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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     837.5
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

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Gapop 10.0 , Gapext 0.5
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       MESSKKMDSPGALQTNPPLK.....IKDDTIFIKVIVDTSDLPDP 568
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US-09-724-6766-84446
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US-09-724-6766-89
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US-60-427-194-89
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US-60-427-6668-116
US-10-197-6668-116
US-10-197-6668-112
US-10-197-6668-112
US-10-197-6668-118
US-09-724-676-84447
US-09-724-676-85182
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Sequence 4, Appli sequence 53797, A Sequence 53797, A Sequence 84446, A Sequence 53796, A Sequence 53796, A Sequence 53796, A Sequence 13796, A Sequence 110, Appli sequence 111, Appli sequence 110, Appli sequence 111, Appli sequence 110, Appli sequence 110, Appli sequence 110, Appli sequence 110, Appli sequence 111, Appli sequence 112, Appli sequence 112, Appli sequence 113, Appli sequence 113, Appli sequence 113, Appli sequence 113, Appli sequence 114, Appli sequence 113, Appli sequence 113, Appli sequence 113, Appli sequence 114, Appli sequence 114, Appli sequence 118, Appli se
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3 SSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKT-VEDKYKCEKCHLVLC 61 :: : | | | | | | :| :|

27.8%; Score 837.5; DB 6; 33.6%; Pred. No. 1.2e-70; ative 89; Mismatches 194;

Indels 105; Gaps

17;

Length

Query Match 27.1 Best Local Similarity 33.1 Matches 196; Conservative

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ULT 1 -10-283-50 Sequence GENERAL GENERAL APP TIT NUM COR PRI ATT INFORMAT SEQ -10-283-50	72226666666666666666666666666666666666
3-500-4 APPLICA TITLE ( NUMBER CORRESS SS COMPUTE SS CO	11111111111111111111111111111111111111
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plication US/10283500 RRMATION: NT: Goeddel, David V. Rothe, Mike F INVENTION: Tumor Ne OF SEQUENCES: 59 ONDENCE ADDRESS: DRESSEE: Genentech, I REET: 460 Point San Francis MINTRY: USA DIMTRY: USA UNTRY: USA DIM TYPE: 3.5 inch, MPUTER: IBM PC compatt ERATING SYSTEM: PC-DO FTWARE: WinDatin (Gen APPLICATION NUMBER: US/ LING DATE: 30-Oct-200 ASSIFICATION NUMBER: US/ LING DATE: 07-Jan-199 MY/AGENT INFORMATION: ME: Dreger, Ginger R. ME: Dreger, Ginger R. ME: DATE: 07-Jan-199 MY/AGENT INFORMATION: ME: A15/25-3216 LEFAX: 415/52-9881 LEFAX: 910/371-7168 FOR SEQ ID NO: 4: E CHARACTERISTICS: NGTH: 501 amino acids PE: Amino Acid PDISCRIPTION: SEQ ID EDESCRIPTION: SEQ ID	ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ ហ
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US-09-724-676-53797; Sequence 53797, Application US/09724676; GENERAL INFORMATION:
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 53797
LENGTH: 519
TYPE: PRT
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                      Matches 175;
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                                        175 PERSISCRHCRAPCCGADVKAHHEV-CPKFPLTC-DGCGKKKIPREKFQDHVKTCGKCRV 232
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231 TCSFKRYGCV--FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK-----VSLLQ 278
                                                                                171 KYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPS 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 REATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTC
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                                                                                                                        122 PAVC--PSDGCTWKGTLKEY-----ESCHEGRCPLMLTECPACKGLVRLGEKERHLEHEC
                                                                                                                                                              114 QIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVR---PDCKEKVLRKDLRDHVEKAC 170
                                                                                                                                                                                                                         63 PKOTECGHRFCESCMAALLSSSSPKCTAC-QESIVKDKV------FKDNCCKREILAL 113
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                                                                                                                                                                                                      PFQAQCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARKGVESL 121
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                    23.2%; Score 696.5; DB 5; 33.1%; Pred. No. 2.4e-57; tive 83; Mismatches 174;
                                                                                                                                                                                                                                                                                                                            Length 519;
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KTATFENIVCVLNREVERKTATFENIVCVLNREVER	171 KYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLL	Query Match 23.2%; Score 696.5; DB 5; Length 519; Best Local Similarity 33.1%; pred. No. 2.4e-57; Matches 175; Conservative 83; Mismatches 174; Indels 97; G  Qy 63 PKOTECGHAPICESCMAALLSSSSPKCTAG-QESIVKDKVFKDNCCKREILAL	-676A-53797 e 53797, Application US/09724676A e INFORMATION: ANT: Compugen LTD OF INVENTION: Variants of alternative splicing EFFERENCE: 129181.4 Compugen T APPLICATION UMBER: US/09/724,676A T FILING DATE: 2000-11-28 OF SEQ ID NOS: 97222 RE: Patentin version 3.2 NO 53797 ISM: Homo sapiens -676A-53797	518		Qy 398 RLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCAR	QY 338 RPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDI	Qy 279 N-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEI	Db 233 PCREHAIGCLETVEGEKQQEHEVQWLREHLAMLLSSVLEAKPLLGDQSHAGSELLQ
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322 397 351	230 232 278 278 288 288 337	ps 20; 113 121 170			517 470	457 411	397 351	337 322	288

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Sequence 84446, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT FILLIG DATE: US/09/724,676A
CURRENT FILLIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 9722
SOFTMARE: Patentin version 3.2
SEQ ID NO 84446
LENGTH: 308
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spiritle REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 308
                                 ; ORGANISM: Homo sapiens US-09-724-676A-84446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKHDTHINIHKAQLSKNEERFKLLEGTCYNGKLIWKVTDYKMKKREAVDGHTVSIFSQSF 184
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 Score 682.5;
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APPLICANT: Compugen LTD
FILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 53796
LENGTH: 536
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-53796
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                                                                                                                                                                                                                                   TCSFKRYGCV--FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK------VSLLQ 278
                                                                                                                                        N-ESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEI 337
                                                                                                                                                                                     PCRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQ
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                                          RPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDI 397
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp.
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 53796
LENGTH: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 QIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVR---PDCKEKVLRKDLRDHVEKAC 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 RLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCAR 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 PFQAQCGHRYCSFCLASILSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARKGVESL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 PKQTECGHRFCESCMAALLSSSSPKCTAC-QESIVKDKV-----FKDNCCKREILAL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocal Similarity
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                                                                                                               SSSFKKPTGEMNIASGCPVFVAQTVLE-NGTYIKDD 552
                                                                                                                                                              IYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVT 470
                                                                                                                                                                                      VYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPN 517
                                                                                                                                                                                                                                                        AMADLEQKVRPFQAQCGHRYCSFCLASILRKLQEAVAGRIPAIFSPAFYTSRYGYKMCLR 411
                                                                                                                                                                                                                                                                                                RLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCAR 457
                                                                                                                                                                                                                                                                                                                                                                                          RPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDI 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCRFHAIGCLETVEGEKQQ--EHEVQWLREHLAML--LSSVLEAKPLLGDQSHAGSELLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
348
                                                                                                                                                                                229 VVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFLWKITNVTKRCHESVCGRTVSLFSPA 288
                                                                                                                                                                                                                                389
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                                                                                                                                                                                                                                                                                                                                                                                                                   278 QNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEK-LKELDKE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 SFKRYGCVFQGTNQQIKAHEASSAVQHVNL----LKEWSNS------LEKKVSLL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 REATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/779,599
FILING DATE: 07-Jan-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 RVLCCTACLSE----NLRDDEDRICPKCRADNLHPVSPGSPLTQE-KVH-SDVAEAEIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA
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                                      RRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDT 562
                                                                                                               FYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLÞWFFKQKVTIMLMDQGSS 504
                                                                                                                                                                                                                            ----DQMLSVHDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQP 444
                                                                                                                                                                                                                                                                                                                          IRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAGYGCSFKGSPQSMQEHEATSQSSHLYLLLAVLKEWKSSPGSNLGSAPMALERNLSEL
REHAIDAFRPDLSSASFQRPQSETNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVDT
                                                                                         FYTAKYGYKLCLRLYLNGDGSGKKTHLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQ-NN
                                                                                                                                                                                                                                                                                                                                                                     Q------LQAAVEATGDLEVDCYRAPCCESQEELALQHLVK-----EKLLAQLEEK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 409 amino acids TYPE: Amino Acid TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/283,500 FILING DATE: 30-Oct-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                            --ANIVAVLNKEVE-----ASHLALAASIHQSQLDREHLLSLEQR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.9%; Score 628; DB 6; Length 409; 36.6%; Pred. No. 4.9e-51;
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Sequence 89, Application US/60427194
GENERAL INFORMATION:
APPLICANT: American Home Products Inc.
APPLICANT: American Home Products Inc.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING SCHIZOPHRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 234
SOFTWARE: PatentIn version 3.1
SEQ ID NO 89
LENGTH: 470
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/60/423,586
CURRENT FILING DATE: 2002-11-05
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING SCHIZOPHRENI
                                                                                                                                                                                       414 WKNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRAAVE
                                                                                                                                                                                                                                                                                                                                                                                                              402 MDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLN 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 QNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 SE-CVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNES 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 LAQHATSECPKRTQPCTYCTKEFVFDTIQSHQYQCPRLPVACPNQCGVGTVAREDLPGHL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KLSRRDLPAHLQHDCPKRRLKCEFCGCDFSGEAYESHEGMCPQESVYCENKCGARMMRRL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 VEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFR 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 KDSCNTALVLCPFKDSGCKHRCPKLAMARHVEESVKPHLAMM------
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es 147; Conservative
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                                                                                                                                                                                                                                  SSSFKKP-----TGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVD 561
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CURRENT APPLICATION NUMBER: US/60/427,194
CURRENT FILING DATE: 2002-11-19
NUMBER OF SEQ ID NOS: 234
SOFTWARE: Patentin version 3.1
SEQ ID NO 89
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Best Local Similarity
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TYPE: PRT
414 WKNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRAAVE
                                                                                                                 462 GDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG----SSRRHLGDAFKPDPN
                                                                                                                                                                                            402 MDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLN
                                                                                                                                                                                                                                                                          342 QNWEEADSMKSSVESLQNRVTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLAD 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 YAKIYPDPELEVQVLGLPIRCIHSEEGCRWSGPLRHLQGHL-NTCSFNVIPC--PNRCPM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 GYKEKFYKTYEDKYKCEKCHLYLCSPKQ-TECGHRFCESCMAALLSSSSPKCTACQESIV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GFDYKFLEKPKRRLLCPLCGKPMREPVQVSTCGHRFCDTCLQEFLSEGVFKCPEDQLPLD 62
                                   SSSFKKP-----TGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVD 561
                                                                           GNGSGEGTHLSLYIRVLPGAFDNLLEWPFARRVTFSLLDQSDPGLAKPQHVTETFHPDPN
                                                                                                                                                                                                                                                                                                                    ------CA-----CA------LVSRQRQELQELRREL----
                                                                                                                                                                                                                                                                                                                                                         VEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFR 341
                                                                                                                                                                                                                                                                                                                                                                                               KDSCNTALVLCPFKDSGCKHRCPKLAMARHVEESVKPHLAMM------
                                                                                                                                                                                                                                                                                                                                                                                                                                       SE-CVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNES 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAQHATSECPKRTQPCTYCTKEFVFDTIQSHQYQCPRLPVACPNQCGVGTVAREDLPGHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLSRRDLPAHLQHDCPKRRLKCEFCGCDFSGEAYESHEGMCPQESVYCENKCGARMMRRL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVLRKDLRDHVEKACKYREATCSHCKSQVPMIALQKHE---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDKVFKDNCCKREILALQIYCRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVRPD-CKE 155
                                                                                                                                                        -------GSDGVLIWKIGSYGRRLQEAKAKPNLECFSPAFYTHKYGYKLQVSAFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.6%; Score 560.5; DB 7; 24.9%; Pred. No. 1.4e-44; tive 75; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 470;
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                                                                             413
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RESULT 11

US-09-716-536-10

; Sequence 10, Application US/09716536

; GENERAL INFORMATION:

APPLICANT: Young Lee

APPLICANT: Yongwon Choi

TITLE OF INVENTION: Signal Transducer for the TNF Receptor

TITLE OF INVENTION: Signal Transducer for the TNF Receptor

FILE REFERENCE: 600-1-198CIPICON

CURRENT APPLICATION NUMBER: US/09/716,536

CURRENT FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 60/042,293

PRIOR FILING DATE: 1997-04-01

PRIOR APPLICATION NUMBER: 60/042,747

PRIOR FILING DATE: 1997-04-07
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RESULT 12
US-10-197-666A-116
(S-10-197-666A-116
; Sequence 116, Application US/10197666A
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSIKI KAISYA
; TITLE OF INVENTION: Elk1 phosphorylation related gene
; FILE REFERENCE: PH-1548US
; CURRENT APPLICATION NUMBER: US/10/197,666A
; CURRENT EILING DATE: 2002-11-18
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PRIOR APPLICATION NUMBER: JP 2001-253450
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: JP 2001-253450
PRIOR APPLICATION NUMBER: JP 2002-012176
PRIOR APPLICATION NUMBER: JP 2002-012176
PRIOR FILING DATE: 2002-01-21
PRIOR APPLICATION NUMBER: US 60/305,884
PRIOR PILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/316,304
PRIOR APPLICATION NUMBER: US 60/316,304
PRIOR FILING DATE: 2001-09-04
PRIOR FILING DATE: 2001-09-04
PRIOR FILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 156
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US-10-197-666A-116
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 46
TYPE: PRT
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SEQ ID NO 116
LENGTH: 631
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.3%;
Best Local Similarity 95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.1%; Score 212.5; DB 6; Length 631; Best Local Similarity 21.3%; Pred. No. 1.4e-11; Matches 102; Conservative 52; Mismatches 166; Indels 159; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: fragment
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                                                    220 CPHSKYGCTFIG-----NQDTYET 238
                                                                                                                                                      189 YRP----- 219
                                                                                                                                                                                                      172 YREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPST 231
                                                                                                                                                                                                                                                                                   100 KDPVITTCGHTFCRRC-----ALKSEKCPV------DN-AKLTVVVNNI----- 136
  292 HNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMK 351
                                                                                                 232 CSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSL 291
                                                                                                                                                                                                                                                        137 --AVAEQ--IGELFIHCRHGCHAAGTGKPGVFEVDP---RGCPFTIKLSARKDH-ESSCD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 KYKCEKCHLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KYKCEKCRLVLCNPKQTECGHRFCESCMAALLSSSSPKCTACQESI 46
                                                                                                                                                                                                                                                                                                                                                                                                             61 CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 TKAADGTGTYKOH----RRTPSSSSTLAYSPRDEEDGMEPLVFAEQPSVKLCCQLCCSVF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SKKMDSPGALQTNPPLKLHTDRSAGTPVFVP---EQGGYKEKFVKTVEDKYKCEKCHLVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 249; DB 5; Length 46; Pred. No. 1.2e-16; 1; Mismatches 1; Indels
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	FLRSMLGKLSEKIDQLEKSLELKFDVLDENQSKLSEDLMEFRRDASMLNDELS 366	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	314	Db	
	SVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLA 400	2 QNWEEADSMKSSVESLQNRVTELE-S	34	Qy	
	EGLKEFLQQTDDR-FHEMHVALAQKDQEIA 313	NQDTYETHLETCRF	271	Дb	
	LHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFR 341	VEKNKSIQS	282	Qy	
	270		251	Db	
	LSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNES 281		222	Qу	
	YRCPNNPSCPPLLKMNLEAH 250	RKDH-ESSCDYRP	219	Db	
	LRDHVEKACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAH 221		162	Qy	
	IGELFIHCRHGCHAAGTGKPGVFEVDPRGCPFTIKLSA 218	VVNNIAVAEQ	171	Db	
	LKNDCHFEELPCVRPDCKEKVLRKD 161	LALQIYCRNESRGCAEQLT	111	Qy	
	ALKSEKCPVDN-AKLTV 170	LCCQLCCSVFKDPVITTCGHTFCRRC-	129	Db	
	AALL	!	53	Qy.	
	PRDEEDGMPPINTPRRSDSAISVRSLHSESSMSLRSTFSLPEEEEEPEPLVFAEQPSVK 128	თ –	69	Db	
	LHTDRSAGTPVFVPEQGGYKEKFVKTVEDKYK 52	- to	4	Qy	
20;	Score 209.5; DB 6; Length 670; Pred. No. 2.9e-11; Formatches 167; Indels 165; Gaps	7.0%; Similarity 21.1%; 3; Conservative	Query Match Best Local Matches 10	H	
		TYPE: PRT ORGANISM: Mus musculus 0-197-666A-114	TYPE: ORGAN 10-197	us;	
		ID NO 114 NGTH: 670	EQI	 &	
		R OF SEQ ID NOS: 156 NRE: PatentIn Ver. 2.1	NUMBER OF SOFTWARE:		
	50,027	R APPLICATION NUMBER: US 60/35 R FILING DATE: 2002-01-23	PRIOR		
	16,304	APPLICATION NUMBER: US 60/31 FILING DATE: 2001-09-04	PRIOR		
	)5,884	2	PRIOR PRIOR	·. ·.	
		FILING DATE: 2002-01-21	PRIOR	·. ·.	
	2002-012176	FILING DATE: 2001-08-31	PRIOR		
	·263450	FILING DATE: 2001-07-18 APPLICATION NUMBER: JP 2001-	PRIOR		
	218204	APPLICATION NUMBER: JP 2001-	PRIOR		
	197,666A		CURRENT		
	ulsiA Plation related gene	ANT: ASAHI KASEI KABUSIKI KAISIA OF INVENTION: EIKI phosphorylation	APPLIC TITLE	٠. ٠.	
	100.	GENERAL INFORMATION:	ENERAL		
	66A	-666A-114	SULT 13 3-10-197	RES	
	TFVGHQGPVWCLCVYSMGDLLFSGS 376	LGSYDPQQIFKCKG	338	DЬ	
	TASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGT 469		411	Оу	
	SMLGKLSEKINQLEKSLELKFDVLDENQSKLSEDLMEFRRDASMLNDELSHINARLNMGI 337	SMLGKLSEKINQLEKSLELKFDVLDEN	278	Db	
	SVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLE 410	SSVESLQNRVTELE-SVDKSAGQVARN	352	Qy	
	EMHVALAQKDQEIAFLR 277	HLETCRFEGLKEFLQQSDDR-FHEMHV-	239	Db	

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PRIOR APPLICATION NUMBER: US/10/197,666A
PRIOR APPLICATION NUMBER: JP 2001-218204
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: JP 2002-012176
PRIOR APPLICATION NUMBER: JP 2002-012176
PRIOR FILING DATE: 2002-01-21
PRIOR FILING DATE: 2002-01-21
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APPLICANT: ASAHI KASEI KABUSIKI KAISYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Pa
SEQ ID NO 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/305,884
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/316,304
PRIOR FILING DATE: 2001-09-04
PRIOR PPLICATION NUMBER: US 60/350,027
PRIOR FILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Elk1 | FILE REFERENCE: PH-1548US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                            416 GVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGT 469
                                                                                        293 LSEKIDQLEKSLELKFDYLDENQSKLSEDLMEFRRDASMLNDELSHINARLNMGILGSYD
                                                                                                                                    357 LQNRVTELE-SVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYN 415
              353 PQQIFKCKG-----
                                                                                                                                                                                  254 RF----EGLKEFLQQTDDR-FHEMHV-----ALAQKDQEIA------FLRSMLGK 292
                                                                                                                                                                                                                               297 SFEIEIEROKEMLRNNESKILHLORVIDSOAEKLKELDKEIRPFRONWEEADSMKSSVES 356
                                                                                                                                                                                                                                                                             235 YGCTFIG-----NQDTYETHLETC 253
                                                                                                                                                                                                                                                                                                                         237 YGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQIC 296
                                                                                                                                                                                                                                                                                                                                                                                                                    177 CSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 VNNIA--VAEQ--IGELFIHCRHGCR-----VAGSGKPPIFEVDPRG----- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 CSVEKDPVITTCGHTECRRC-----ALKSEKCPV------DN-----VKLTVV 142
                                                                                                                                                                                                                                                                                                                                                                        181 --- CPFTIKLSARKDHEGS-CDYRPVRCPNNPSCPPLLRMNLEAHLKECEHI--KCPHSK 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 CRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 HLVLCSPKQTECGHRECESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 ISTPRRSDSAISVRS-----LHSESSMSLRSTFSLPEEEEEPEPLVFAEQPSVKLCCQLC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 MGDLLFSGS 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MESSKKMDSPGALQTNPPLKLHTDRSAG--TPVFVPEQGGYKEKFVKTVEDKYK--CEKC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HINARLNMGILGSYDPQQIFKCKG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9%; Score 207.5; DB 6; Length 641; 21.1%; Pred. No. 4.2e-11; ative 61; Mismatches 170; Indels 143
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-----TFVGHQGPVWCLCVYSMGDLLFSGS 386
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US-10-197-666A-150
Sequence 150, Applic
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/197,666A CURRENT FILING DATE: 2002-11-18 PRIOR APPLICATION NUMBER: JP 2001-218204 PRIOR EILING DATE: 2001-07-18 PRIOR APPLICATION NUMBER: JP 2001-263450 PRIOR APPLICATION NUMBER: JP 2001-263450 PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ASAHI KASEI KABUSIKI KAISYA
TITLE OF INVENTION: Elkl phosphorylation related gene
FILE REFERENCE: PH-1548US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/305,884 PRIOR FILING DATE: 2001-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2002-012176
PRIOR FILING DATE: 2002-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/350,027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 670
                                            416 GVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGT 469
          382 PQQIFKCKG
                                                                                              322 LSEKIDQLEKSLELKFDYLDENQSKLSEDLMEFRRDASMLNDELSHINARLNMGILGSYD
                                                                                                                                           357 LQNRVTELE-SYDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYN 415
                                                                                                                                                                                             283 RF----EGLKEFLQQTDDR-FHEMHV-----ALAQKDQEIA------FLRSMLGK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 VNNIA--VAEQ--IGELFIHCRHGCR-----VAGSGKPPIFEVDPRG------ 209
                                                                                                                                                                                                                                                            297
                                                                                                                                                                                                                                                                                                              264
                                                                                                                                                                                                                                                                                                                                                                                               210 ---CPFTIKLSARKDHEGS-CDYRPVRCPNNPSCPPLLRMNLEAHLKECEHI--KCPHSK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                               177 CSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKR 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 CRNESRGCAEQLTLGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 CSVFKDPVITTCGHTFCRRC-----ALKSEKCPV-------DN-----VKLTVV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 HLVLCSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 ISTPRRSDSAISVRS-----LHSESSMSLRSTFSLPEEEEEPEPLVFAEQPSVKLCCQLC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MESSKKMDSPGALQTNPPLKLHTDRSAG--TPVFVPEQGGYKEKFVKTVEDKYK--CEKC 56
                                                                                                                                                                                                                                               SFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVES 356
                                                                                                                                                                                                                                                                                                              YGCTFIG-----
                                                                                                                                                                                                                                                                                                                                             YGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQIC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 61; Mismatches 170; Indels 143; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10197666A
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--TFVGHQGPVWCLCVYSMGDLLFSGS 415
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Search completed: December 19, 2002, 14:59:20 Job time : 21 secs

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